

# SEQUENCE LISTING

<110> Nicolaides, Nicholas C  
Grasso, Luigi  
Sass, Philip M

<120> CHEMICAL INHIBITORS OF MISMATCH REPAIR

<130> MOR-0017

<140> 00/000,000

<141> 2001-01-15

<160> 44

<170> PatentIn Ver. 2.1

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<211> 52

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide  
primer

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<223> Description of Artificial Sequence:oligonucleotide  
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taagtcttaa gtgctaccaa c 21

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<211> 53

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<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide  
primer

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<223> Description of Artificial Sequence:oligonucleotide  
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<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 5

ctgatctcac ggacaatagt gc 22

<210> 6

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<223> Description of Artificial Sequence:oligonucleotide  
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ggctccataa aaagtcacc 20

<210> 7

<211> 22  
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primer

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22

<210> 8  
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<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 8  
atcttgaaac ctttagggag gg

22

<210> 9  
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primer

<400> 9  
agaagtttag acaggtac

18

<210> 10  
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<223> Description of Artificial Sequence:oligonucleotide  
primer

<400> 10

aaatgtgcaa ttgccttc

18

<210> 11

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<212> DNA

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<223> Description of Artificial Sequence:oligonucleotide  
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<400> 11

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<211> 48

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide  
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<400> 12

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48

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<211> 30

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:oligonucleotide  
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<210> 14

<211> 859

<212> PRT

<213> Mus musculus

<400> 14

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 35 40 45  
 Ala Gly Ala Thr Thr Ile Asp Leu Arg Leu Lys Asp Tyr Gly Val Asp  
 50 55 60  
 Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Glu Asn Phe  
 65 70 75 80  
 Glu Gly Leu Ala Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
 85 90 95  
 Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
 100 105 110  
 Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Gly Ser  
 115 120 125  
 Ala Ser Val Gly Thr Arg Leu Val Phe Asp His Asn Gly Lys Ile Thr  
 130 135 140  
 Gln Lys Thr Pro Tyr Pro Arg Pro Lys Gly Thr Thr Val Ser Val Gln  
 145 150 155 160  
 His Leu Phe Tyr Thr Leu Pro Val Arg Tyr Lys Glu Phe Gln Arg Asn  
 165 170 175  
 Ile Lys Lys Glu Tyr Ser Lys Met Val Gln Val Leu Gln Ala Tyr Cys  
 180 185 190  
 Ile Ile Ser Ala Gly Val Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
 195 200 205  
 Gly Lys Arg His Ala Val Val Cys Thr Ser Gly Thr Ser Gly Met Lys  
 210 215 220  
 Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
 225 230 235 240  
 Pro Phe Val Gln Leu Pro Pro Ser Asp Ala Val Cys Glu Glu Tyr Gly  
 245 250 255

Leu Ser Thr Ser Gly Arg His Lys Thr Phe Ser Thr Phe Arg Ala Ser  
260 265 270

Phe His Ser Ala Arg Thr Ala Pro Gly Gly Val Gln Gln Thr Gly Ser  
275 280 285

Phe Ser Ser Ser Ile Arg Gly Pro Val Thr Gln Gln Arg Ser Leu Ser  
290 295 300

Leu Ser Met Arg Phe Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
305 310 315 320

Val Val Leu Asn Val Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
325 330 335

Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
340 345 350

Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Ala Asn  
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Lys Leu Asn Val Asn Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
370 375 380

Val Lys Leu His Thr Ala Glu Leu Glu Lys Pro Val Pro Gly Lys Gln  
385 390 395 400

Asp Asn Ser Pro Ser Leu Lys Ser Thr Ala Asp Glu Lys Arg Val Ala  
405 410 415

Ser Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu His Pro Thr Lys Glu  
420 425 430

Ile Lys Ser Arg Gly Pro Glu Thr Ala Glu Leu Thr Arg Ser Phe Pro  
435 440 445

Ser Glu Lys Arg Gly Val Leu Ser Ser Tyr Pro Ser Asp Val Ile Ser  
450 455 460

Tyr Arg Gly Leu Arg Gly Ser Gln Asp Lys Leu Val Ser Pro Thr Asp  
465 470 475 480

Ser Pro Gly Asp Cys Met Asp Arg Glu Lys Ile Glu Lys Asp Ser Gly  
485 490 495

Leu Ser Ser Thr Ser Ala Gly Ser Glu Glu Glu Phe Ser Thr Pro Glu  
500 505 510

Val Ala Ser Ser Phe Ser Ser Asp Tyr Asn Val Ser Ser Leu Glu Asp  
515 520 525

Arg Pro Ser Gln Glu Thr Ile Asn Cys Gly Asp Leu Asp Cys Arg Pro  
530 535 540

Pro Gly Thr Gly Gln Ser Leu Lys Pro Glu Asp His Gly Tyr Gln Cys  
545 550 555 560

Lys Ala Leu Pro Leu Ala Arg Leu Ser Pro Thr Asn Ala Lys Arg Phe  
565 570 575

Lys Thr Glu Glu Arg Pro Ser Asn Val Asn Ile Ser Gln Arg Leu Pro  
580 585 590

Gly Pro Gln Ser Thr Ser Ala Ala Glu Val Asp Val Ala Ile Lys Met  
595 600 605

Asn Lys Arg Ile Val Leu Leu Glu Phe Ser Leu Ser Ser Leu Ala Lys  
610 615 620

Arg Met Lys Gln Leu Gln His Leu Lys Ala Gln Asn Lys His Glu Leu  
625 630 635 640

Ser Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu Asn Gln Ala  
645 650 655

Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Ser Met Phe Ala Glu  
660 665 670

Met Glu Ile Leu Gly Gln Phe Asn Leu Gly Phe Ile Val Thr Lys Leu  
675 680 685

Lys Glu Asp Leu Phe Leu Val Asp Gln His Ala Ala Asp Glu Lys Tyr  
690 695 700

Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Ala Gln Arg Leu  
705 710 715 720

Ile Thr Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu Ala Val Leu  
725 730 735

Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp Phe Val Ile  
740 745 750

Asp Glu Asp Ala Pro Val Thr Glu Arg Ala Lys Leu Ile Ser Leu Pro  
755 760 765

Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Ile Asp Glu Leu Ile  
770 775 780

Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro Ser Arg Val  
785 790 795 800

Arg Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val Met Ile Gly  
805 810 815

Thr Ala Leu Asn Ala Ser Glu Met Lys Lys Leu Ile Thr His Met Gly  
820 825 830

Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro Thr Met Arg  
835 840 845

His Val Ala Asn Leu Asp Val Ile Ser Gln Asn  
850 855

<210> 15

<211> 3056

<212> DNA

<213> Mus musculus

<400> 15

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gtcttttccc gagagcgcca ccgcaactct ccgcggtga ctgtgactgg aggagtcctg 180  
catccatgga gcaaacggaa ggcgtgagta cagaatgtgc taaggccatc aagcctattg 240  
atgggaagtc agtccatcaa atttgttctg ggcaggtgat actcagtta agcaccgcgtg 300  
tgaaggagtt gatagaaaa atgtgtagatg ctgttgctac tactattgat ctaaggctta 360  
aagactatgg ggtggacctc attgaagttt cagacaatgg atgtggggta gaagaagaaa 420  
actttgaagg tctagctctg aaacatcaca catctaagat tcaagagttt gcgcacctca 480  
cgcaggttga aactttcggc ttctgggggg aagctctgag ctctctgtgt gcaactaagtg 540  
atgtcactat atctacctgc cacgggtctg caagcgttgg gactcgactg gtgtttgacc 600  
ataatgggaa aatcaccgca aaaactccct acccccagacc taaaggaacc acagtcagtg 660  
tgacgacactt attttataca ctaccocgtgc gttacaaaaga gtttcagagg aacattaaaa 720  
aggagtattc caaaatggtg caggtcttac aggcgtactg tatcatctca gcaggcgtcc 780  
gtgtaagctg cactaatcag ctccggacag ggaagcggca cgctgtggtg tgcacaagcg 840  
gcacgtctgg catgaaggaa aatatcgggt ctgtgtttgg ccagaagcag ttgcaaaaggc 900  
tcattccctt tggtcagctg cccctagtg acgtgtgtg tgaagagtac ggcctgagca 960  
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ataaaagcca aattctacta caagaagaga agctattgct ggccgtttta aagacctcct 1260  
tgataggaa gtgtgacagt gatgcaaaac agcttaattg caaccagcag ccaactgctag 1320  
atgttgaagg taacttagta aagctgcata ctgcagaact agaaaagcct gtgccaggaa 1380





Leu Ile Glu Val Ser Asp Asn Gly Cys Gly Val Glu Glu Asn Phe  
 65 70 75 80

Glu Gly Leu Thr Leu Lys His His Thr Ser Lys Ile Gln Glu Phe Ala  
 85 90 95

Asp Leu Thr Gln Val Glu Thr Phe Gly Phe Arg Gly Glu Ala Leu Ser  
 100 105 110

Ser Leu Cys Ala Leu Ser Asp Val Thr Ile Ser Thr Cys His Ala Ser  
 115 120 125

Ala Lys Val Gly Thr Arg Leu Met Phe Asp His Asn Gly Lys Ile Ile  
 130 135 140

Gln Lys Thr Pro Tyr Pro Arg Pro Arg Gly Thr Thr Val Ser Val Gln  
 145 150 155 160

Gln Leu Phe Ser Thr Leu Pro Val Arg His Lys Glu Phe Gln Arg Asn  
 165 170 175

Ile Lys Lys Glu Tyr Ala Lys Met Val Gln Val Leu His Ala Tyr Cys  
 180 185 190

Ile Ile Ser Ala Gly Ile Arg Val Ser Cys Thr Asn Gln Leu Gly Gln  
 195 200 205

Gly Lys Arg Gln Pro Val Val Cys Thr Gly Gly Ser Pro Ser Ile Lys  
 210 215 220

Glu Asn Ile Gly Ser Val Phe Gly Gln Lys Gln Leu Gln Ser Leu Ile  
 225 230 235 240

Pro Phe Val Gln Leu Pro Pro Ser Asp Ser Val Cys Glu Glu Tyr Gly  
 245 250 255

Leu Ser Cys Ser Asp Ala Leu His Asn Leu Phe Tyr Ile Ser Gly Phe  
 260 265 270

Ile Ser Gln Cys Thr His Gly Val Gly Arg Ser Ser Thr Asp Arg Gln  
 275 280 285

Phe Phe Phe Ile Asn Arg Arg Pro Cys Asp Pro Ala Lys Val Cys Arg  
 290 295 300

Leu Val Asn Glu Val Tyr His Met Tyr Asn Arg His Gln Tyr Pro Phe  
 305 310 315 320

Val Val Leu Asn Ile Ser Val Asp Ser Glu Cys Val Asp Ile Asn Val  
 325 330 335  
 Thr Pro Asp Lys Arg Gln Ile Leu Leu Gln Glu Glu Lys Leu Leu Leu  
 340 345 350  
 Ala Val Leu Lys Thr Ser Leu Ile Gly Met Phe Asp Ser Asp Val Asn  
 355 360 365  
 Lys Leu Asn Val Ser Gln Gln Pro Leu Leu Asp Val Glu Gly Asn Leu  
 370 375 380  
 Ile Lys Met His Ala Ala Asp Leu Glu Lys Pro Met Val Glu Lys Gln  
 385 390 395 400  
 Asp Gln Ser Pro Ser Leu Arg Thr Gly Glu Glu Lys Lys Asp Val Ser  
 405 410 415  
 Ile Ser Arg Leu Arg Glu Ala Phe Ser Leu Arg His Thr Thr Glu Asn  
 420 425 430  
 Lys Pro His Ser Pro Lys Thr Pro Glu Pro Arg Arg Ser Pro Leu Gly  
 435 440 445  
 Gln Lys Arg Gly Met Leu Ser Ser Ser Thr Ser Gly Ala Ile Ser Asp  
 450 455 460  
 Lys Gly Val Leu Arg Pro Gln Lys Glu Ala Val Ser Ser Ser His Gly  
 465 470 475 480  
 Pro Ser Asp Pro Thr Asp Arg Ala Glu Val Glu Lys Asp Ser Gly His  
 485 490 495  
 Gly Ser Thr Ser Val Asp Ser Glu Gly Phe Ser Ile Pro Asp Thr Gly  
 500 505 510  
 Ser His Cys Ser Ser Glu Tyr Ala Ala Ser Ser Pro Gly Asp Arg Gly  
 515 520 525  
 Ser Gln Glu His Val Asp Ser Gln Glu Lys Ala Pro Glu Thr Asp Asp  
 530 535 540  
 Ser Phe Ser Asp Val Asp Cys His Ser Asn Gln Glu Asp Thr Gly Cys  
 545 550 555 560  
 Lys Phe Arg Val Leu Pro Gln Pro Thr Asn Leu Ala Thr Pro Asn Thr  
 565 570 575

Lys Arg Phe Lys Lys Glu Glu Ile Leu Ser Ser Ser Asp Ile Cys Gln  
 580 585 590  
 Lys Leu Val Asn Thr Gln Asp Met Ser Ala Ser Gln Val Asp Val Ala  
 595 600 605  
 Val Lys Ile Asn Lys Lys Val Val Pro Leu Asp Phe Ser Met Ser Ser  
 610 615 620  
 Leu Ala Lys Arg Ile Lys Gln Leu His His Glu Ala Gln Gln Ser Glu  
 625 630 635 640  
 Gly Glu Gln Asn Tyr Arg Lys Phe Arg Ala Lys Ile Cys Pro Gly Glu  
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 Asn Gln Ala Ala Glu Asp Glu Leu Arg Lys Glu Ile Ser Lys Thr Met  
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 Phe Ala Glu Met Glu Ile Ile Gly Gln Phe Asn Leu Gly Phe Ile Ile  
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 Thr Lys Leu Asn Glu Asp Ile Phe Ile Val Asp Gln His Ala Thr Asp  
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 Glu Lys Tyr Asn Phe Glu Met Leu Gln Gln His Thr Val Leu Gln Gly  
 705 710 715 720  
 Gln Arg Leu Ile Ala Pro Gln Thr Leu Asn Leu Thr Ala Val Asn Glu  
 725 730 735  
 Ala Val Leu Ile Glu Asn Leu Glu Ile Phe Arg Lys Asn Gly Phe Asp  
 740 745 750  
 Phe Val Ile Asp Glu Asn Ala Pro Val Thr Glu Arg Ala Lys Leu Ile  
 755 760 765  
 Ser Leu Pro Thr Ser Lys Asn Trp Thr Phe Gly Pro Gln Asp Val Asp  
 770 775 780  
 Glu Leu Ile Phe Met Leu Ser Asp Ser Pro Gly Val Met Cys Arg Pro  
 785 790 795 800  
 Ser Arg Val Lys Gln Met Phe Ala Ser Arg Ala Cys Arg Lys Ser Val  
 805 810 815  
 Met Ile Gly Thr Ala Leu Asn Thr Ser Glu Met Lys Lys Leu Ile Thr  
 820 825 830

His Met Gly Glu Met Asp His Pro Trp Asn Cys Pro His Gly Arg Pro  
835 840 845

Thr Met Arg His Ile Ala Asn Leu Gly Val Ile Ser Gln Asn  
850 855 860

<210> 17

<211> 2771

<212> DNA

<213> Homo sapiens

<400> 17

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caagagtttg ccgacctaac tcaggttgaa acttttggct ttcgggggga agctctgagc 360  
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<210> 18

<211> 932

<212> PRT

<213> Homo sapiens

<400> 18

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 20 25 30

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly  
 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val  
 50 55 60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser  
 65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala  
 85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr  
 100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His  
 115 120 125

Ile Leu Ser Gln Lys Pro Ser His Leu Gly Gln Gly Thr Thr Val Thr  
 130 135 140

Ala Leu Arg Leu Phe Lys Asn Leu Pro Val Arg Lys Gln Phe Tyr Ser

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	165			170		175
Met Ser Phe Gly Ile Leu Lys Pro Asp Leu Arg Ile Val Phe Val His						
	180			185		190
Asn Lys Ala Val Ile Trp Gln Lys Ser Arg Val Ser Asp His Lys Met						
	195			200		205
Ala Leu Met Ser Val Leu Gly Thr Ala Val Met Asn Asn Met Glu Ser						
	210			215		220
Phe Gln Tyr His Ser Glu Glu Ser Gln Ile Tyr Leu Ser Gly Phe Leu						
	225			230		235
Pro Lys Cys Asp Ala Asp His Ser Phe Thr Ser Leu Ser Thr Pro Glu						
	245			250		255
Arg Ser Phe Ile Phe Ile Asn Ser Arg Pro Val His Gln Lys Asp Ile						
	260			265		270
Leu Lys Leu Ile Arg His His Tyr Asn Leu Lys Cys Leu Lys Glu Ser						
	275			280		285
Thr Arg Leu Tyr Pro Val Phe Phe Leu Lys Ile Asp Val Pro Thr Ala						
	290			295		300
Asp Val Asp Val Asn Leu Thr Pro Asp Lys Ser Gln Val Leu Leu Gln						
	305			310		315
Asn Lys Glu Ser Val Leu Ile Ala Leu Glu Asn Leu Met Thr Thr Cys						
	325			330		335
Tyr Gly Pro Leu Pro Ser Thr Asn Ser Tyr Glu Asn Asn Lys Thr Asp						
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Val Ser Ala Ala Asp Ile Val Leu Ser Lys Thr Ala Glu Thr Asp Val						
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Leu Phe Asn Lys Val Glu Ser Ser Gly Lys Asn Tyr Ser Asn Val Asp						
	370			375		380
Thr Ser Val Ile Pro Phe Gln Asn Asp Met His Asn Asp Glu Ser Gly						
	385			390		395
Lys Asn Thr Asp Asp Cys Leu Asn His Gln Ile Ser Ile Gly Asp Phe						

405

410

415

Gly Tyr Gly His Cys Ser Ser Glu Ile Ser Asn Ile Asp Lys Asn Thr  
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 435 440 445

Ser Gln Thr Glu Tyr Ser Lys Thr Cys Phe Ile Ser Ser Val Lys His  
 450 455 460

Thr Gln Ser Glu Asn Gly Asn Lys Asp His Ile Asp Glu Ser Gly Glu  
 465 470 475 480

Asn Glu Glu Glu Ala Gly Leu Glu Asn Ser Ser Glu Ile Ser Ala Asp  
 485 490 495

Glu Trp Ser Arg Gly Asn Ile Leu Lys Asn Ser Val Gly Glu Asn Ile  
 500 505 510

Glu Pro Val Lys Ile Leu Val Pro Glu Lys Ser Leu Pro Cys Lys Val  
 515 520 525

Ser Asn Asn Asn Tyr Pro Ile Pro Glu Gln Met Asn Leu Asn Glu Asp  
 530 535 540

Ser Cys Asn Lys Lys Ser Asn Val Ile Asp Asn Lys Ser Gly Lys Val  
 545 550 555 560

Thr Ala Tyr Asp Leu Leu Ser Asn Arg Val Ile Lys Lys Pro Met Ser  
 565 570 575

Ala Ser Ala Leu Phe Val Gln Asp His Arg Pro Gln Phe Leu Ile Glu  
 580 585 590

Asn Pro Lys Thr Ser Leu Glu Asp Ala Thr Leu Gln Ile Glu Glu Leu  
 595 600 605

Trp Lys Thr Leu Ser Glu Glu Glu Lys Leu Lys Tyr Glu Glu Lys Ala  
 610 615 620

Thr Lys Asp Leu Glu Arg Tyr Asn Ser Gln Met Lys Arg Ala Ile Glu  
 625 630 635 640

Gln Glu Ser Gln Met Ser Leu Lys Asp Gly Arg Lys Lys Ile Lys Pro  
 645 650 655

Thr Ser Ala Trp Asn Leu Ala Gln Lys His Lys Leu Lys Thr Ser Leu



660

665

670

Ser Asn Gln Pro Lys Leu Asp Glu Leu Leu Gln Ser Gln Ile Glu Lys  
675 680 685

Arg Arg Ser Gln Asn Ile Lys Met Val Gln Ile Pro Phe Ser Met Lys  
690 695 700

Asn Leu Lys Ile Asn Phe Lys Lys Gln Asn Lys Val Asp Leu Glu Glu  
705 710 715 720

Lys Asp Glu Pro Cys Leu Ile His Asn Leu Arg Phe Pro Asp Ala Trp  
725 730 735

Leu Met Thr Ser Lys Thr Glu Val Met Leu Leu Asn Pro Tyr Arg Val  
740 745 750

Glu Glu Ala Leu Leu Phe Lys Arg Leu Leu Glu Asn His Lys Leu Pro  
755 760 765

Ala Glu Pro Leu Glu Lys Pro Ile Met Leu Thr Glu Ser Leu Phe Asn  
770 775 780

Gly Ser His Tyr Leu Asp Val Leu Tyr Lys Met Thr Ala Asp Asp Gln  
785 790 795 800

Arg Tyr Ser Gly Ser Thr Tyr Leu Ser Asp Pro Arg Leu Thr Ala Asn  
805 810 815

Gly Phe Lys Ile Lys Leu Ile Pro Gly Val Ser Ile Thr Glu Asn Tyr  
820 825 830

Leu Glu Ile Glu Gly Met Ala Asn Cys Leu Pro Phe Tyr Gly Val Ala  
835 840 845

Asp Leu Lys Glu Ile Leu Asn Ala Ile Leu Asn Arg Asn Ala Lys Glu  
850 855 860

Val Tyr Glu Cys Arg Pro Arg Lys Val Ile Ser Tyr Leu Glu Gly Glu  
865 870 875 880

Ala Val Arg Leu Ser Arg Gln Leu Pro Met Tyr Leu Ser Lys Glu Asp  
885 890 895

Ile Gln Asp Ile Ile Tyr Arg Met Lys His Gln Phe Gly Asn Glu Ile  
900 905 910

Lys Glu Cys Val His Gly Arg Pro Phe Phe His His Leu Thr Tyr Leu

Pro Glu Thr Thr  
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<211> 3063  
<212> DNA  
<213> Homo sapiens

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atgctggtgc cacaagcgta gatgttaaac tggagaacta tggatttgat aaaattgagg 240  
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atctctcat gagctttgggt atccttaaac ctgacttaag gattgtcttt gtacataaca 660  
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 aac 3063

<210> 20

<211> 934

<212> PRT

<213> Homo sapiens

<400> 20

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 35 40 45  
 Asp Ala Leu Leu Ala Ala Arg Glu Val Phe Lys Thr Gln Gly Val Ile  
 50 55 60  
 Lys Tyr Met Gly Pro Ala Gly Ala Lys Asn Leu Gln Ser Val Val Leu  
 65 70 75 80  
 Ser Lys Met Asn Phe Glu Ser Phe Val Lys Asp Leu Leu Leu Val Arg  
 85 90 95  
 Gln Tyr Arg Val Glu Val Tyr Lys Asn Arg Ala Gly Asn Lys Ala Ser  
 100 105 110  
 Lys Glu Asn Asp Trp Tyr Leu Ala Tyr Lys Ala Ser Pro Gly Asn Leu  
 115 120 125

Ser Gln Phe Glu Asp Ile Leu Phe Gly Asn Asn Asp Met Ser Ala Ser  
130 135 140

Ile Gly Val Val Gly Val Lys Met Ser Ala Val Asp Gly Gln Arg Gln  
145 150 155 160

Val Gly Val Gly Tyr Val Asp Ser Ile Gln Arg Lys Leu Gly Leu Cys  
165 170 175

Glu Phe Pro Asp Asn Asp Gln Phe Ser Asn Leu Glu Ala Leu Leu Ile  
180 185 190

Gln Ile Gly Pro Lys Glu Cys Val Leu Pro Gly Gly Glu Thr Ala Gly  
195 200 205

Asp Met Gly Lys Leu Arg Gln Ile Ile Gln Arg Gly Gly Ile Leu Ile  
210 215 220

Thr Glu Arg Lys Lys Ala Asp Phe Ser Thr Lys Asp Ile Tyr Gln Asp  
225 230 235 240

Leu Asn Arg Leu Leu Lys Gly Lys Lys Gly Glu Gln Met Asn Ser Ala  
245 250 255

Val Leu Pro Glu Met Glu Asn Gln Val Ala Val Ser Ser Leu Ser Ala  
260 265 270

Val Ile Lys Phe Leu Glu Leu Leu Ser Asp Asp Ser Asn Phe Gly Gln  
275 280 285

Phe Glu Leu Thr Thr Phe Asp Phe Ser Gln Tyr Met Lys Leu Asp Ile  
290 295 300

Ala Ala Val Arg Ala Leu Asn Leu Phe Gln Gly Ser Val Glu Asp Thr  
305 310 315 320

Thr Gly Ser Gln Ser Leu Ala Ala Leu Leu Asn Lys Cys Lys Thr Pro  
325 330 335

Gln Gly Gln Arg Leu Val Asn Gln Trp Ile Lys Gln Pro Leu Met Asp  
340 345 350

Lys Asn Arg Ile Glu Glu Arg Leu Asn Leu Val Glu Ala Phe Val Glu  
355 360 365

Asp Ala Glu Leu Arg Gln Thr Leu Gln Glu Asp Leu Leu Arg Arg Phe  
370 375 380

Pro Asp Leu Asn Arg Leu Ala Lys Lys Phe Gln Arg Gln Ala Ala Asn  
 385 390 395 400  
 Leu Gln Asp Cys Tyr Arg Leu Tyr Gln Gly Ile Asn Gln Leu Pro Asn  
 405 410 415  
 Val Ile Gln Ala Leu Glu Lys His Glu Gly Lys His Gln Lys Leu Leu  
 420 425 430  
 Leu Ala Val Phe Val Thr Pro Leu Thr Asp Leu Arg Ser Asp Phe Ser  
 435 440 445  
 Lys Phe Gln Glu Met Ile Glu Thr Thr Leu Asp Met Asp Gln Val Glu  
 450 455 460  
 Asn His Glu Phe Leu Val Lys Pro Ser Phe Asp Pro Asn Leu Ser Glu  
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 515 520 525  
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 Glu Glu Tyr Thr Lys Asn Lys Thr Glu Tyr Glu Glu Ala Gln Asp Ala  
 565 570 575  
 Ile Val Lys Glu Ile Val Asn Ile Ser Ser Gly Tyr Val Glu Pro Met  
 580 585 590  
 Gln Thr Leu Asn Asp Val Leu Ala Gln Leu Asp Ala Val Val Ser Phe  
 595 600 605  
 Ala His Val Ser Asn Gly Ala Pro Val Pro Tyr Val Arg Pro Ala Ile  
 610 615 620  
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 625 630 635 640

Cys Val Glu Val Gln Asp Glu Ile Ala Phe Ile Pro Asn Asp Val Tyr  
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 Phe Glu Lys Asp Lys Gln Met Phe His Ile Ile Thr Gly Pro Asn Met  
 660 665 670  
 Gly Gly Lys Ser Thr Tyr Ile Arg Gln Thr Gly Val Ile Val Leu Met  
 675 680 685  
 Ala Gln Ile Gly Cys Phe Val Pro Cys Glu Ser Ala Glu Val Ser Ile  
 690 695 700  
 Val Asp Cys Ile Leu Ala Arg Val Gly Ala Gly Asp Ser Gln Leu Lys  
 705 710 715 720  
 Gly Val Ser Thr Phe Met Ala Glu Met Leu Glu Thr Ala Ser Ile Leu  
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 Arg Ser Ala Thr Lys Asp Ser Leu Ile Ile Ile Asp Glu Leu Gly Arg  
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 Gly Thr Ser Thr Tyr Asp Gly Phe Gly Leu Ala Trp Ala Ile Ser Glu  
 755 760 765  
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 770 775 780  
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 785 790 795 800  
 His Val Thr Ala Leu Thr Thr Glu Glu Thr Leu Thr Met Leu Tyr Gln  
 805 810 815  
 Val Lys Lys Gly Val Cys Asp Gln Ser Phe Gly Ile His Val Ala Glu  
 820 825 830  
 Leu Ala Asn Phe Pro Lys His Val Ile Glu Cys Ala Lys Gln Lys Ala  
 835 840 845  
 Leu Glu Leu Glu Glu Phe Gln Tyr Ile Gly Glu Ser Gln Gly Tyr Asp  
 850 855 860  
 Ile Met Glu Pro Ala Ala Lys Lys Cys Tyr Leu Glu Arg Glu Gln Gly  
 865 870 875 880  
 Glu Lys Ile Ile Gln Glu Phe Leu Ser Lys Val Lys Gln Met Pro Phe  
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Thr Glu Met Ser Glu Glu Asn Ile Thr Ile Lys Leu Lys Gln Leu Lys  
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915 920 925

Arg Ile Lys Val Thr Thr  
930

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<211> 3145  
<212> DNA  
<213> Homo sapiens

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<211> 756

<212> PRT

<213> Homo sapiens

<400> 22

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 Lys Glu Met Ile Glu Asn Cys Leu Asp Ala Lys Ser Thr Ser Ile Gln  
 35 40 45  
 Val Ile Val Lys Glu Gly Leu Lys Leu Ile Gln Ile Gln Asp Asn  
 50 55 60  
 Gly Thr Gly Ile Arg Lys Glu Asp Leu Asp Ile Val Cys Glu Arg Phe  
 65 70 75 80  
 Thr Thr Ser Lys Leu Gln Ser Phe Glu Asp Leu Ala Ser Ile Ser Thr  
 85 90 95  
 Tyr Gly Phe Arg Gly Glu Ala Leu Ala Ser Ile Ser His Val Ala His



100	105	110
Val Thr Ile Thr Thr Lys Thr Ala Asp Gly Lys Cys Ala Tyr Arg Ala 115	120	125
Ser Tyr Ser Asp Gly Lys Leu Lys Ala Pro Pro Lys Pro Cys Ala Gly 130	135	140
Asn Gln Gly Thr Gln Ile Thr Val Glu Asp Leu Phe Tyr Asn Ile Ala 145	150	155
Thr Arg Arg Lys Ala Leu Lys Asn Pro Ser Glu Glu Tyr Gly Lys Ile 165	170	175
Leu Glu Val Val Gly Arg Tyr Ser Val His Asn Ala Gly Ile Ser Phe 180	185	190
Ser Val Lys Lys Gln Gly Glu Thr Val Ala Asp Val Arg Thr Leu Pro 195	200	205
Asn Ala Ser Thr Val Asp Asn Ile Arg Ser Ile Phe Gly Asn Ala Val 210	215	220
Ser Arg Glu Leu Ile Glu Ile Gly Cys Glu Asp Lys Thr Leu Ala Phe 225	230	235
Lys Met Asn Gly Tyr Ile Ser Asn Ala Asn Tyr Ser Val Lys Lys Cys 245	250	255
Ile Phe Leu Leu Phe Ile Asn His Arg Leu Val Glu Ser Thr Ser Leu 260	265	270
Arg Lys Ala Ile Glu Thr Val Tyr Ala Ala Tyr Leu Pro Lys Asn Thr 275	280	285
His Pro Phe Leu Tyr Leu Ser Leu Glu Ile Ser Pro Gln Asn Val Asp 290	295	300
Val Asn Val His Pro Thr Lys His Glu Val His Phe Leu His Glu Glu 305	310	315
Ser Ile Leu Glu Arg Val Gln Gln His Ile Glu Ser Lys Leu Leu Gly 325	330	335
Ser Asn Ser Ser Arg Met Tyr Phe Thr Gln Thr Leu Leu Pro Gly Leu 340	345	350
Ala Gly Pro Ser Gly Glu Met Val Lys Ser Thr Thr Ser Leu Thr Ser		

365

Glu Tyr Ile Val Glu Phe Leu Lys Lys Lys Ala Glu Met Leu Ala Asp

610

615

620

Tyr Phe Ser Leu Glu Ile Asp Glu Glu Gly Asn Leu Ile Gly Leu Pro  
625 630 635 640

Leu Leu Ile Asp Asn Tyr Val Pro Pro Leu Glu Gly Leu Pro Ile Phe  
645 650 655

Ile Leu Arg Leu Ala Thr Glu Val Asn Trp Asp Glu Glu Lys Glu Cys  
660 665 670

Phe Glu Ser Leu Ser Lys Glu Cys Ala Met Phe Tyr Ser Ile Arg Lys  
675 680 685

Gln Tyr Ile Ser Glu Glu Ser Thr Leu Ser Gly Gln Gln Ser Glu Val  
690 695 700

Pro Gly Ser Ile Pro Asn Ser Trp Lys Trp Thr Val Glu His Ile Val  
705 710 715 720

Tyr Lys Ala Leu Arg Ser His Ile Leu Pro Pro Lys His Phe Thr Glu  
725 730 735

Asp Gly Asn Ile Leu Gln Leu Ala Asn Leu Pro Asp Leu Tyr Lys Val  
740 745 750

Phe Glu Arg Cys  
755

&lt;210&gt; 23

&lt;211&gt; 2484

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 23

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gttaaaaaac aaggagagac agtagctgat gttaggacac tacccaatgc ctcaaccgtg 660  
gacaatatct gctccatctt tggaatgct gttagtgcag aactgataga aattggatgt 720

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<212> PRT

<213> Homo sapiens

<400> 24

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Ile Ile Thr Ser Val Val Ser Val Val Lys Glu Leu Ile Glu Asn Ser  
 20 25 30

Leu Asp Ala Gly Ala Thr Ser Val Asp Val Lys Leu Glu Asn Tyr Gly  
 35 40 45

Phe Asp Lys Ile Glu Val Arg Asp Asn Gly Glu Gly Ile Lys Ala Val

50

55

60

Asp Ala Pro Val Met Ala Met Lys Tyr Tyr Thr Ser Lys Ile Asn Ser  
65 70 75 80

His Glu Asp Leu Glu Asn Leu Thr Thr Tyr Gly Phe Arg Gly Glu Ala  
85 90 95

Leu Gly Ser Ile Cys Cys Ile Ala Glu Val Leu Ile Thr Thr Arg Thr  
100 105 110

Ala Ala Asp Asn Phe Ser Thr Gln Tyr Val Leu Asp Gly Ser Gly His  
115 120 125

Ile Leu Ser Gln Lys  
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&lt;210&gt; 25

&lt;211&gt; 426

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

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acttga 426

&lt;210&gt; 26

&lt;211&gt; 1360

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 26

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1 5 10 15

Leu Ser Asp Ala Asn Lys Ala Ser Ala Arg Ala Ser Arg Glu Gly Gly  
20 25 30

Arg Ala Ala Ala Ala Pro Gly Ala Ser Pro Ser Pro Gly Gly Asp Ala  
35 40 45

Ala Trp Ser Glu Ala Gly Pro Gly Pro Arg Pro Leu Ala Arg Ser Ala  
 50 55 60  
 Ser Pro Pro Lys Ala Lys Asn Leu Asn Gly Gly Leu Arg Arg Ser Val  
 65 70 75 80  
 Ala Pro Ala Ala Pro Thr Ser Cys Asp Phe Ser Pro Gly Asp Leu Val  
 85 90 95  
 Trp Ala Lys Met Glu Gly Tyr Pro Trp Trp Pro Cys Leu Val Tyr Asn  
 100 105 110  
 His Pro Phe Asp Gly Thr Phe Ile Arg Glu Lys Gly Lys Ser Val Arg  
 115 120 125  
 Val His Val Gln Phe Phe Asp Asp Ser Pro Thr Arg Gly Trp Val Ser  
 130 135 140  
 Lys Arg Leu Leu Lys Pro Tyr Thr Gly Ser Lys Ser Lys Glu Ala Gln  
 145 150 155 160  
 Lys Gly Gly His Phe Tyr Ser Ala Lys Pro Glu Ile Leu Arg Ala Met  
 165 170 175  
 Gln Arg Ala Asp Glu Ala Leu Asn Lys Asp Lys Ile Lys Arg Leu Glu  
 180 185 190  
 Leu Ala Val Cys Asp Glu Pro Ser Glu Pro Glu Glu Glu Glu Met  
 195 200 205  
 Glu Val Gly Thr Thr Tyr Val Thr Asp Lys Ser Glu Glu Asp Asn Glu  
 210 215 220  
 Ile Glu Ser Glu Glu Glu Val Gln Pro Lys Thr Gln Gly Ser Arg Arg  
 225 230 235 240  
 Ser Ser Arg Gln Ile Lys Lys Arg Arg Val Ile Ser Asp Ser Glu Ser  
 245 250 255  
 Asp Ile Gly Gly Ser Asp Val Glu Phe Lys Pro Asp Thr Lys Glu Glu  
 260 265 270  
 Gly Ser Ser Asp Glu Ile Ser Ser Gly Val Gly Asp Ser Glu Ser Glu  
 275 280 285  
 Gly Leu Asn Ser Pro Val Lys Val Ala Arg Lys Arg Lys Arg Met Val  
 290 295 300

Thr Gly Asn Gly Ser Leu Lys Arg Lys Ser Ser Arg Lys Glu Thr Pro  
 305 310 315 320  
 Ser Ala Thr Lys Gln Ala Thr Ser Ile Ser Ser Glu Thr Lys Asn Thr  
 325 330 335  
 Leu Arg Ala Phe Ser Ala Pro Gln Asn Ser Glu Ser Gln Ala His Val  
 340 345 350  
 Ser Gly Gly Gly Asp Asp Ser Ser Arg Pro Thr Val Trp Tyr His Glu  
 355 360 365  
 Thr Leu Glu Trp Leu Lys Glu Glu Lys Arg Arg Asp Glu His Arg Arg  
 370 375 380  
 Arg Pro Asp His Pro Asp Phe Asp Ala Ser Thr Leu Tyr Val Pro Glu  
 385 390 395 400  
 Asp Phe Leu Asn Ser Cys Thr Pro Gly Met Arg Lys Trp Trp Gln Ile  
 405 410 415  
 Lys Ser Gln Asn Phe Asp Leu Val Ile Cys Tyr Lys Val Gly Lys Phe  
 420 425 430  
 Tyr Glu Leu Tyr His Met Asp Ala Leu Ile Gly Val Ser Glu Leu Gly  
 435 440 445  
 Leu Val Phe Met Lys Gly Asn Trp Ala His Ser Gly Phe Pro Glu Ile  
 450 455 460  
 Ala Phe Gly Arg Tyr Ser Asp Ser Leu Val Gln Lys Gly Tyr Lys Val  
 465 470 475 480  
 Ala Arg Val Glu Gln Thr Glu Thr Pro Glu Met Met Glu Ala Arg Cys  
 485 490 495  
 Arg Lys Met Ala His Ile Ser Lys Tyr Asp Arg Val Val Arg Arg Glu  
 500 505 510  
 Ile Cys Arg Ile Ile Thr Lys Gly Thr Gln Thr Tyr Ser Val Leu Glu  
 515 520 525  
 Gly Asp Pro Ser Glu Asn Tyr Ser Lys Tyr Leu Leu Ser Leu Lys Glu  
 530 535 540  
 Lys Glu Glu Asp Ser Ser Gly His Thr Arg Ala Tyr Gly Val Cys Phe  
 545 550 555 560

Val	Asp	Thr	Ser	Leu	Gly	Lys	Phe	Phe	Ile	Gly	Gln	Phe	Ser	Asp	Asp	
				565					570					575		
Arg	His	Cys	Ser	Arg	Phe	Arg	Thr	Leu	Val	Ala	His	Tyr	Pro	Pro	Val	
				580				585					590			
Gln	Val	Leu	Phe	Glu	Lys	Gly	Asn	Leu	Ser	Lys	Glu	Thr	Lys	Thr	Ile	
		595					600					605				
Leu	Lys	Ser	Ser	Leu	Ser	Cys	Ser	Leu	Gln	Glu	Gly	Leu	Ile	Pro	Gly	
	610					615					620					
Ser	Gln	Phe	Trp	Asp	Ala	Ser	Lys	Thr	Leu	Arg	Thr	Leu	Leu	Glu	Glu	
625					630					635				640		
Glu	Tyr	Phe	Arg	Glu	Lys	Leu	Ser	Asp	Gly	Ile	Gly	Val	Met	Leu	Pro	
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Gln	Val	Leu	Lys	Gly	Met	Thr	Ser	Glu	Ser	Asp	Ser	Ile	Gly	Leu	Thr	
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Pro	Gly	Glu	Lys	Ser	Glu	Leu	Ala	Leu	Ser	Ala	Leu	Gly	Gly	Cys	Val	
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Phe	Tyr	Leu	Lys	Lys	Cys	Leu	Ile	Asp	Gln	Glu	Leu	Leu	Ser	Met	Ala	
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Asn	Phe	Glu	Glu	Tyr	Ile	Pro	Leu	Asp	Ser	Asp	Thr	Val	Ser	Thr	Thr	
705					710					715				720		
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Ala	Val	Thr	Leu	Asn	Asn	Leu	Glu	Ile	Phe	Leu	Asn	Gly	Thr	Asn	Gly	
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Ser	Thr	Glu	Gly	Thr	Leu	Leu	Glu	Arg	Val	Asp	Thr	Cys	His	Thr	Pro	
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Phe	Gly	Lys	Arg	Leu	Leu	Lys	Gln	Trp	Leu	Cys	Ala	Pro	Leu	Cys	Asn	
	770					775					780					
His	Tyr	Ala	Ile	Asn	Asp	Arg	Leu	Asp	Ala	Ile	Glu	Asp	Leu	Met	Val	
785					790					795				800		
Val	Pro	Asp	Lys	Ile	Ser	Glu	Val	Val	Glu	Leu	Leu	Lys	Lys	Leu	Pro	
				805					810					815		





Pro Met Cys Arg Pro Val Ile Leu Leu Pro Glu Asp Thr Pro Pro Phe  
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Leu Glu Leu Lys Gly Ser Arg His Pro Cys Ile Thr Lys Thr Phe Phe  
1090 1095 1100

Gly Asp Asp Phe Ile Pro Asn Asp Ile Leu Ile Gly Cys Glu Glu Glu  
1105 1110 1115 1120

Glu Gln Glu Asn Gly Lys Ala Tyr Cys Val Leu Val Thr Gly Pro Asn  
1125 1130 1135

Met Gly Gly Lys Ser Thr Leu Met Arg Gln Ala Gly Leu Leu Ala Val  
1140 1145 1150

Met Ala Gln Met Gly Cys Tyr Val Pro Ala Glu Val Cys Arg Leu Thr  
1155 1160 1165

Pro Ile Asp Arg Val Phe Thr Arg Leu Gly Ala Ser Asp Arg Ile Met  
1170 1175 1180

Ser Gly Glu Ser Thr Phe Phe Val Glu Leu Ser Glu Thr Ala Ser Ile  
1185 1190 1195 1200

Leu Met His Ala Thr Ala His Ser Leu Val Leu Val Asp Glu Leu Gly  
1205 1210 1215

Arg Gly Thr Ala Thr Phe Asp Gly Thr Ala Ile Ala Asn Ala Val Val  
1220 1225 1230

Lys Glu Leu Ala Glu Thr Ile Lys Cys Arg Thr Leu Phe Ser Thr His  
1235 1240 1245

Tyr His Ser Leu Val Glu Asp Tyr Ser Gln Asn Val Ala Val Arg Leu  
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Gly His Met Ala Cys Met Val Glu Asn Glu Cys Glu Asp Pro Ser Gln  
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Glu Thr Ile Thr Phe Leu Tyr Lys Phe Ile Lys Gly Ala Cys Pro Lys  
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Ser Tyr Gly Phe Asn Ala Ala Arg Leu Ala Asn Leu Pro Glu Glu Val  
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Ile Gln Lys Gly His Arg Lys Ala Arg Glu Phe Glu Lys Met Asn Gln  
1315 1320 1325

Ser Leu Arg Leu Phe Arg Glu Val Cys Leu Ala Ser Glu Arg Ser Thr  
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<212> DNA  
<213> Homo sapiens

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 <211> 1128  
 <212> PRT  
 <213> Homo sapiens

<400> 28

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Ser Leu Lys Ser Thr Ser Ser Ser Thr Gly Ala Ala Asp Gln Val Asp  
35 40 45

Pro Gly Ala Ala Ala Ala Ala Ala Pro Pro Ala Pro Ala Phe Pro Pro  
50 55 60

Gln Leu Pro Pro His Val Ala Thr Glu Ile Asp Arg Arg Lys Lys Arg  
65 70 75 80

Pro Leu Glu Asn Asp Gly Pro Val Lys Lys Lys Val Lys Lys Val Gln  
85 90 95

Gln Lys Glu Gly Gly Ser Asp Leu Gly Met Ser Gly Asn Ser Glu Pro  
100 105 110

Lys Lys Cys Leu Arg Thr Arg Asn Val Ser Lys Ser Leu Glu Lys Leu  
115 120 125

Lys Glu Phe Cys Cys Asp Ser Ala Leu Pro Gln Ser Arg Val Gln Thr  
130 135 140

Glu Ser Leu Gln Glu Arg Phe Ala Val Leu Pro Lys Cys Thr Asp Phe  
145 150 155 160

Asp Asp Ile Ser Leu Leu His Ala Lys Asn Ala Val Ser Ser Glu Asp  
165 170 175

Ser Lys Arg Gln Ile Asn Gln Lys Asp Thr Thr Leu Phe Asp Leu Ser  
180 185 190

Gln Phe Gly Ser Ser Asn Thr Ser His Glu Asn Leu Gln Lys Thr Ala  
195 200 205

Ser Lys Ser Ala Asn Lys Arg Ser Lys Ser Ile Tyr Thr Pro Leu Glu  
210 215 220

Leu Gln Tyr Ile Glu Met Lys Gln Gln His Lys Asp Ala Val Leu Cys  
225 230 235 240

Val Glu Cys Gly Tyr Lys Tyr Arg Phe Phe Gly Glu Asp Ala Glu Ile  
245 250 255

Ala Ala Arg Glu Leu Asn Ile Tyr Cys His Leu Asp His Asn Phe Met  
 260 265 270  
 Thr Ala Ser Ile Pro Thr His Arg Leu Phe Val His Val Arg Arg Leu  
 275 280 285  
 Val Ala Lys Gly Tyr Lys Val Gly Val Val Lys Gln Thr Glu Thr Ala  
 290 295 300  
 Ala Leu Lys Ala Ile Gly Asp Asn Arg Ser Ser Leu Phe Ser Arg Lys  
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 Leu Thr Ala Leu Tyr Thr Lys Ser Thr Leu Ile Gly Glu Asp Val Asn  
 325 330 335  
 Pro Leu Ile Lys Leu Asp Asp Ala Val Asn Val Asp Glu Ile Met Thr  
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 Asp Thr Ser Thr Ser Tyr Leu Leu Cys Ile Ser Glu Asn Lys Glu Asn  
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 Val Arg Asp Lys Lys Lys Gly Asn Ile Phe Ile Gly Ile Val Gly Val  
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 420 425 430  
 Arg Ala Thr Ser Val Ser Val Gln Asp Asp Arg Ile Arg Val Glu Arg  
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 Met Asp Asn Ile Tyr Phe Glu Tyr Ser His Ala Phe Gln Ala Val Thr  
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 Glu Phe Tyr Ala Lys Asp Thr Val Asp Ile Lys Gly Ser Gln Ile Ile  
 465 470 475 480  
 Ser Gly Ile Val Asn Leu Glu Lys Pro Val Ile Cys Ser Leu Ala Ala  
 485 490 495  
 Ile Ile Lys Tyr Leu Lys Glu Phe Asn Leu Glu Lys Met Leu Ser Lys  
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Pro Glu Asn Phe Lys Gln Leu Ser Ser Lys Met Glu Phe Met Thr Ile  
 515 520 525

Asn Gly Thr Thr Leu Arg Asn Leu Glu Ile Leu Gln Asn Gln Thr Asp  
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Met Lys Thr Lys Gly Ser Leu Leu Trp Val Leu Asp His Thr Lys Thr  
 545 550 555 560

Ser Phe Gly Arg Arg Lys Leu Lys Lys Trp Val Thr Gln Pro Leu Leu  
 565 570 575

Lys Leu Arg Glu Ile Asn Ala Arg Leu Asp Ala Val Ser Glu Val Leu  
 580 585 590

His Ser Glu Ser Ser Val Phe Gly Gln Ile Glu Asn His Leu Arg Lys  
 595 600 605

Leu Pro Asp Ile Glu Arg Gly Leu Cys Ser Ile Tyr His Lys Lys Cys  
 610 615 620

Ser Thr Gln Glu Phe Phe Leu Ile Val Lys Thr Leu Tyr His Leu Lys  
 625 630 635 640

Ser Glu Phe Gln Ala Ile Ile Pro Ala Val Asn Ser His Ile Gln Ser  
 645 650 655

Asp Leu Leu Arg Thr Val Ile Leu Glu Ile Pro Glu Leu Leu Ser Pro  
 660 665 670

Val Glu His Tyr Leu Lys Ile Leu Asn Glu Gln Ala Ala Lys Val Gly  
 675 680 685

Asp Lys Thr Glu Leu Phe Lys Asp Leu Ser Asp Phe Pro Leu Ile Lys  
 690 695 700

Lys Arg Lys Asp Glu Ile Gln Gly Val Ile Asp Glu Ile Arg Met His  
 705 710 715 720

Leu Gln Glu Ile Arg Lys Ile Leu Lys Asn Pro Ser Ala Gln Tyr Val  
 725 730 735

Thr Val Ser Gly Gln Glu Phe Met Ile Glu Ile Lys Asn Ser Ala Val  
 740 745 750

Ser Cys Ile Pro Thr Asp Trp Val Lys Val Gly Ser Thr Lys Ala Val  
 755 760 765

Ser Arg Phe His Ser Pro Phe Ile Val Glu Asn Tyr Arg His Leu Asn  
770 775 780

Gln Leu Arg Glu Gln Leu Val Leu Asp Cys Ser Ala Glu Trp Leu Asp  
785 790 795 800

Phe Leu Glu Lys Phe Ser Glu His Tyr His Ser Leu Cys Lys Ala Val  
805 810 815

His His Leu Ala Thr Val Asp Cys Ile Phe Ser Leu Ala Lys Val Ala  
820 825 830

Lys Gln Gly Asp Tyr Cys Arg Pro Thr Val Gln Glu Glu Arg Lys Ile  
835 840 845

Val Ile Lys Asn Gly Arg His Pro Val Ile Asp Val Leu Leu Gly Glu  
850 855 860

Gln Asp Gln Tyr Val Pro Asn Asn Thr Asp Leu Ser Glu Asp Ser Glu  
865 870 875 880

Arg Val Met Ile Ile Thr Gly Pro Asn Met Gly Gly Lys Ser Ser Tyr  
885 890 895

Ile Lys Gln Val Ala Leu Ile Thr Ile Met Ala Gln Ile Gly Ser Tyr  
900 905 910

Val Pro Ala Glu Glu Ala Thr Ile Gly Ile Val Asp Gly Ile Phe Thr  
915 920 925

Arg Met Gly Ala Ala Asp Asn Ile Tyr Lys Gly Arg Ser Thr Phe Met  
930 935 940

Glu Glu Leu Thr Asp Thr Ala Glu Ile Ile Arg Lys Ala Thr Ser Gln  
945 950 955 960

Ser Leu Val Ile Leu Asp Glu Leu Gly Arg Gly Thr Ser Thr His Asp  
965 970 975

Gly Ile Ala Ile Ala Tyr Ala Thr Leu Glu Tyr Phe Ile Arg Asp Val  
980 985 990

Lys Ser Leu Thr Leu Phe Val Thr His Tyr Pro Pro Val Cys Glu Leu  
995 1000 1005

Glu Lys Asn Tyr Ser His Gln Val Gly Asn Tyr His Met Gly Phe Leu  
1010 1015 1020



Val Ser Glu Asp Glu Ser Lys Leu Asp Pro Gly Ala Ala Glu Gln Val  
1025 1030 1035 1040

Pro Asp Phe Val Thr Phe Leu Tyr Gln Ile Thr Arg Gly Ile Ala Ala  
1045 1050 1055

Arg Ser Tyr Gly Leu Asn Val Ala Lys Leu Ala Asp Val Pro Gly Glu  
1060 1065 1070

Ile Leu Lys Lys Ala Ala His Lys Ser Lys Glu Leu Glu Gly Leu Ile  
1075 1080 1085

Asn Thr Lys Arg Lys Arg Leu Lys Tyr Phe Ala Lys Leu Trp Thr Met  
1090 1095 1100

His Asn Ala Gln Asp Leu Gln Lys Trp Thr Glu Glu Phe Asn Met Glu  
1105 1110 1115 1120

Glu Thr Gln Thr Ser Leu Leu His  
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<212> DNA

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